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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
      Pred. No. is t
score greater
                                                                                                                                                                                                     1242
864.5
834
768.5
606.5
                                                                                                        88
87.5
87
86.5
                                                                                                                                          89.5
89
88.5
88.5
     82
82
                            83
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                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                           seq
                                                                                                                                                                                                                                                                                                        derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                                     100.0
69.6
67.1
61.9
48.8
48.8
                                                                                                                                                                                                                                                                                                   is the number of results predicted by chance to have ater than or equal to the score of the result being provided by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 hits satisfying chosen parameters:
                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                       Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283224 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTVLAPAWSPTTYLLLLLLL......RPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-994-468-6
1242
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                            PIR_73:*
     Copyright
                                                                                                                                                                                                                                                                                                                                        p1r1:*
p1r2:*
p1r3:*
p1r4:*
                                                                                                                                                                                                                                                              Length
                                                                               1386
753
479
910
590
299
485
746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapext 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using sw model
  T19800
I36948
                           A39283
E75630
A45690
                                                                    T17832
A33647
T28004
A87646
                                                                                                                                                         I48201
S60735
                                                                                                                                                                           TNBE12
T19543
                                                                                                                                                                                           I58343
T22672
                                                                                                                                                                                                                                     I38440
S43293
                                                                                                       A40437
                                                                                                                                          T00257
                                                                                                                                                  AB1990
                                                                                                                                                                                                                                                             Ħ
                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search time 19 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (without alignments)
1189.031 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                  283224
hypothetical prote
Ig epsilon-chain -
               hypothetical prote
                        hypothetical prote
                                gamma-glutamyl car
hypothetical prote
                                                  tegument protein
                                                         hypothetical prote
hypothetical prote
Fc gamma (IgG) rec
                                                                                                    tyrosine kinase re
glutamic acid-rich
                                                                                                                               hypothetical prote OP protein - Kenne
                                                                                                                                                       hypothétical prote
adhalin - golden h
splicing factor SF
                                                                                   sulfated surface g
                                                                                                                     protein-tyrosine-p
                                                                                                                                                                                                FLT3/FLK2 ligand (flt3 ligand isofor
                                                                                             hypothetical prote
                                                                                                                                                                                                                                                           Description
                                                                                                                                               hypothetical
                                                                                                                                                                                                                 Flt3 ligand
flt3/flk-2 ]
                                                                                                                                                                                                                                   flt3 ligand
FLT3/FLK2 l
                                                                                                                                                                                4K alapha trans-in
                                                                                                                                                                                         ypothetical prote
                                                                                                                                                                                                                                                                                                            printed,
                                                                                                                                                                                                                 ligand
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4 4	442	38 40	35 36 37	333 433	30 31
80.5	80.5 80.5	81 81 81	81.5 81.5	82 82 81.5	82.5 82.5
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1176 1306	388 428 636	· 196 209 294	488 958 1119	106 854 485	512 513
NN	2 1 2	N N N		พพพฺ	NN
T49482 T13592	S15591 EHHU JW0047	B48232 A48232 A12016	S13423 T13593	T06479 T23837 C75460	D40829
hypothetical prote hypothetical prote	probable transposa Ig epsilon chain C class I cytokinase	cysteine-rich exte cysteine-rich exte hypothetical prote	stromelyal grote hypothetical prote related to cytoske	proline/leucine-ri hypothetical prote hypothetical prote	ívin

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A;Introns: 11/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNĀ
A;Residues: 1-71'A',73-235 <HAN>
A;Cross-references: GB:U04806; NII:g483844; PIDN:AAA17999.1; PID:g483845
A;Note: the authors translated the codon AGT for residue 25 as Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368, 643-648, 1994

A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopot A;Reference number: S43290; MUID:94195428; PMID:8145851

A;Accession: S43292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escoboncogene 11, 1165-1172, 1995

A;Title: Structural analysis of human and murine flt3 ligand genomic loci.
A;Reference number: 139075; MUID:96032581; PMID:7566977

A;Accession: 139075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flt3 ligand - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C;Accession: I38440; I39075; S43292
R;Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe Blood 83, 2795-2801, 1994
A;Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo A;Reference number: I38440; MUID:94235842; PMID:8180375
A;Accession: I38440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037 R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.E.; felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U03858; NID:g494978; PIDN:AAA19825.1; PID:g494979 R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-235 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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Best Local S
Matches 235
                                     121
                                                                                         61
                                                                                                                                       61
                                                                                                                                                                                                              1 MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                         ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                                                                                                   MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                           ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-235 <RE2>
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                               100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                      48/3; 66/3; 114/3; 161/1; 220/3
                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                            Score 1242;
Pred. No. 5.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                          DB 2;
.4e-99;
.s 0;
                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                          Gaps
                                                                              120
                           180
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Q
                                                                                                                                    C;Genetics:
A;Introns: 11/3; 48/3;
                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-178 < RES>
                                                                                                                                                                                                                                           C;Accession: I39076
R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, Oncogene 11, 1165-1172, 1995
A;Title: Structural analysis of human and murine flt3 ligand genomic loci.
A;Reference number: I39075; MUID:96032581; PMID:7566977
A;Accession: I39076
                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-245 <HAN>
A;Note: the authors translated the codon AGT for residue 25 as Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
$43293
FLT3/FLK2 ligand (clone S109)
C;Species: Homo sapiens (man)
C;Date: 20-Oct.1994 #sequence
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Nature 368, 643-648, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Hannum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S43293
                                                                                                                                                                                                                                                                                                                                                                                      Flt3 ligand alternatively spliced isoform – human
                                                                                                                                                                     Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 WPRPHPGEDTEAHRGESP------ARGCIAWTQRKLARGRSLPWAPLIPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASNIQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                             MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APQP-----PLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVOTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPGA---PRPQSPGPAACGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176;
                                                                                 Similarity
                                                                67.1%; Score 834; Dilarity 100.0%; Pred. No. 3.: Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                      66/3; 114/3; 161/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.6%;
73.0%;
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Pred. No. 1.2e-66;
                                                                                                                                                                                                                             GB/EMBL/DDB.
                                                                               3.3e-64;
                                                                                                   DB 2;
                                                                                                 Length 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          irawski, S.; Bazan, J.F.;
Roncarolo, M.G.; Zlotnik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                     PID:g1072038
                                                                0,
                                                            Gaps
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                       7 60
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                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          Matches
                                                                                                                  61
                                                                                                                                                     60
                                                                LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT 177
                                                                                                                                                                                                       MTVLAPAWSP-TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
       APTAPQPP---LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                            LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                              VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                  MTVLAPAWSPNSSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                            163;
                                                                                                                                                                                                                                                          Conservative
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17;

Mismatches

Indels

9,

Gaps

4

60

120 119

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A; Residues: 1-197,'L',198-231 <HAN>
A; Experimental source: clone T110
A; Note: the sequence from Fig. 2c is inconsistent with C; Genetics:
A; Introns: 11/3; 49/3; 67/3; 115/3; 164/1: 224/3
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040 R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazz felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Nature 368, 643-648, 1994
A:Title: Title: A; Title: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates A;Reference number: S43290; MUID:94195428; PMID:8145851 A;Accession: S43290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-163, 'G', 165, 'HYAG' <RES>
A; Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1;
A; Accession: I49346
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D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
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C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: A49265; I49347; I49346; S43290
C:Accession: A49265; I49347; I49346; S43290
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flt3/flk-2 ligand precursor - mouse
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A; Residues: 1-197, 'L', 198-231 <RE2>
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61.9%; Score 768.5; DB 70.3%; Pred. No. 1.8e-58
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A;Residues: 1-220 <RES>
A;Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1;
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A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopolet A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43291
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felt, A.; Mu
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C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
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$43291
FLT3/FLK2 ligand (clone Tll8) - mouse
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;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
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                                    LREVOINISRLLQETSEQLVALKPWITR -- QNFSRCLELQCQPDSSTLPPPWSPRP----
                                                                    VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                       VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTBIHFVTKCAFQPPPSC
          LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG----
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Pred. No. 1.3e
8; Mismatches
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Pred. No. 1.3e-44;
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C;Superfamily: herpesvirus 77K alpha trans-inducing protein
C;Keywords: trans-inducing protein; transcription regulation
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C;Date: 15-Oc
C;Accession:
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A; Residues: 1-661 <DAV>
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J. Gen. Virol. 67, 1759-1816, 1986
                                                                                                                                                                                                                                                                                                                                                                                             C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                    74K alpha trans-inducing protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
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submitted to the EMBL Data Library,
**Reference number: Z19597
                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                A; Accession: C27342
                                                                                                                                                                                                                                                                                                                             A; Reference number:
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A; Introns: 742/2; 826/1;
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;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *te;
;Accession: T22672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 MERLKTVAGSKMQGL---LERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLV 139
                          GLWRLVLAQRWMERLKTVAGSKMQGLLERVN----TEIHFVTKCAFQP---PPSCLRFV 123
                                                                                          LLSSGLSGTQDCS----FQHSPISSDFAVKI--RELSDYLLQDYPVTVASNLQDEELCG- 71
GLW-WVYENTYWQYLKYTTGAEVPVTSEKVNKKSKSTVLLFSSVVANKPISRHPFKSKVI
                                                              LTSPVLQSTERHSVLLGLHHNNVPESLVVSCMSNDVHDGFMQRYMETIQRCLDDLKLSGD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALKPWITRONFSRCLELOCOPDSSTL---PPPWSPRPLEATAPTAP----OPPLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL----FFASYASNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALRPQPTTSDPTAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATRLTATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LEATAPTAPQPPLLL-----LLLLPVGLLLLAA
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                           te DNA sequence of varicella-zoster A27345; MUID:86306657; PMID:3018124
                                                                                                                                                                                                                                                            EMBL: x04370; NID: g59989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -AWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                7.4%;
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                                                                                                                                              Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93; DB 2
Pred. No. 8;
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               November
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                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                            PIDN:CAA27895.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN: CAB04464.1;
                                                                                                                              103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68;
                                                                                                                                                            Length 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781
                                                                                                                              Indels
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                                                                                                                                                                                                                                                            PID:960001
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                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191
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CESP:F

11;

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adhalin - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
C:Accession: I48201
                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C28D4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19543
                                              A; Cross-relevence. _____C; Superfamily: mouse adhalin
                                                                                                                    A;Title: Adhalin mRNA and cDNA sequence are normal in the A;Reference number: I48201; MUID:95278335; PMID:7758576 A;Accession: I48201
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: T19543
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                                                                                                                                                                                 R;Roberds, S.L.; Campbell, K.P. FEBS Lett. 364, 245-249, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                           RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;McMurray,
                                                                   Molecule type: mRNA; Residues: 1-387 <RES>; Cross-references: EMBL: U21677;
               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Experimental source: clone C28D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-474 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: CESP:C28D4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                    230
                                                                                                                                                                                                                                                                                                                                                                                                    223
                                                                                                                                                                                                                                                                                                                                                                                                                                 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 GYGWMLWFLDVVD-----ARVCRHLKLQFRRIRGPRASV----IPDDLL 287
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
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                                                                                                                                                                                                                                                                                                                                                                    LLLVE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDYPVTVASNLQDEELCGGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKIEEF--RIRAITGG-MSNLLFLVELPAH-LTPIQMEPEKALLRVHCQSDIDQLLSESV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLR-FVQTNISRLLQET- 134
                                                                                                                                                                                                                                                                                                                                       ITVAQ
                                                                                                                                                                                                                                                                                                                                                                                                    PKEPQ--
                                                                                                                                                                                                                                                                                                                                                                                                                            PTAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTP---RPGE-----QVPPVPSPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFTLLSERNLGPKMLGVFPGGRFEQFIPSRALQCLEISKPGLSKLIAPIVARVHTLDAPI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SEQLVALKPWITRONFSRCLELQC----QPDSSTLPPPWSPR--PLEATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPPLLLLLLPVGLLLLAAAWCLHWQRTRRTPRPGEQVPPVPSPQDLL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSDYRGICQELREALGAVQKYM---YFMR-----PDDPTNPSPDTRIRVQEIAAYTAT
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                                                                                                                                                                                                                                                                                                                                       271
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, 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.2%; Score 89.5; Dilarity 24.1%; Pred. No. 5.5; Conservative 29; Mismatches
            7.28;
23.48;
                                                                                                                                                                                                                                                                                                                                                                                               TLQTARQWLERF----KKEPAGERPIEMYLTQAKVPKSDYPST 266
                                                                       NID: 9726481; PIDN: AAA81645.1;
            Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             November 1996
            DB 2;
4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                         Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                              cardiomyopathic hamster.
                                                                       PID: g726482
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                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB:SF3A120; PRP21; SAP114
                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: S60735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing factor SF3a 120K chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :Molecule type: mRNA
:Residues: 1-793 <KRA>
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                         537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 LDQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 LVEH 235
                                                                                                                                                                              64
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                                                                                                                                                                                                                                                                                      Local
                                                    ----TRQNF--SRCLELQCQP----
                                                                                                                 VTKCA-----FQPPPSCLRF---
                                                                                                                                                                            LQDEELCGGLWRLVLAQRWME-RLKTV------
                                                                                                                                                                                                            LPPAPAPDEYLV-
                                                                                                                                                                                                                                                                      67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71;
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                                                                                                                                                                                                                                                                                    22.3%;
                                                                                                                                                                                                                                                                                    7.2%; Score 89; 22.3%; Pred. No.
                                                                                                                                                                                                                                                                    ; Pred. No. 11; 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                    DB
11;
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A;Cross references: GDB:9955873
A;Map position: 22q12.1-22qter
C;Superfamily: human splicing factor SF3a 120K chain; ubiquitin C;Keywords: pre-mRNA splicing
F;714-790/Domain: ubiquitin homology <UBH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S60735; S60733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 51-62;82-94;270-275;397-414;448-463 < KRA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1; PID:g899298
A;Accession: S60733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Mammalian splicing factor SF3al20 represents a A; Reference number: S60733; MUID:96079958; PMID:7489498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 MATSDIOMVHHCTIHGNTEELRQMAARREVPRPLSTLPMFNVRTGERLPPRVDSAQVPLI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 GILEHDPFFCPPTEATGRDFLADALVTLLVPLLVALLL---TLLLAYIMCCRREGQLKRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 SSTLPPPWSPRPLEAT-----APTAPOPPLLLLLLPVGLLLLAAAWC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 CAFQPPP--SC-----LRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 GGLWRL-----VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVT----
                                                                                                                                                                                                                                                                                                                                                                                                                   4 LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
                                                                                                              VEETAIGKKIGEEEIQKPEEKVTWDGHSGSMARTQQAAQANIT--LQEQIEAIHKAKGLV
PEDDTKEKIGPSKPNEIPQQPPPPSSATNIPSSAPPITSVPRPPTMPPPVRTTVVSAVPV
                                                                                                                                                                                                                                        MQEHMRIG-----LLDPRWLEQRDRSIREKQSDDEVYAPGLDIESSLKQLAER-RTDIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAQGQPPLLSCYDSLAPHFRVDWCNVSLVDKSVPEPLD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTRORLLLLI-----EDPEGPRLPYQAEFLVRSHDVEEVL----PSTPANRFL--TAL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC 70
                                                                                                                                                                                                                                                                                                                                                            -----SPITGE---KI---
                                                             -DSSTLP-----PPWSPRPLEAT----APT 180
                                                                                                                                                                              -----VQTNISRLLQETSEQLVALKPWI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79;
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                                                                                                                                                                                                                                                                                               -AGSKMQGLLERVNTEIHF 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 110;
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                                                                                                                                                                                                                                                                                                                                                            -----PASK 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
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A; Experimental source: brain C; Genetics: A; Note: KIAA0476
                                                                                                                                                                                                                                                            R;Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; DNA Res. 4, 345-349, 1997

A;Title: Characterization of cDNA clones in size-fractionated A;Reference number: Z14085; MUID:98116662; PMID:9455484
A;Accession: T00257
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                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1386 <SEK>
                                                                                                                                                                                                                                                                                                                                                    C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change Aj-Jul-2000
C:Accession: T00257
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein KIAA0476 - C; Species: Homo saniene 'man'
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A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB1990
                                                                                                                                                                                                                                         A; Status: preliminary; translated
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C; Accession: AB1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-238 <KUR>
A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein all1471 [imported] - Nostoc
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                            Cross-references: EMBL:AB007945;
                                                                                                                                                                                                                                                                                                                                                  Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: Nostoc sp. strain PCC 7120 is a Date: 14-Dec-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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            1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 GLLLLAAAWCLHWORTRRRTPRPGEQVPPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132
                                    21 SSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC----GGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
          SAGASGSKDAPVPGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVALKPWITRQNFSRCLELQCQPDSSTLPPPW---SPRPLEATAPTAPQPPLLLLLLLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQ------ETSEQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSPISSDFAVKIRELSDYLLQDY---PVTVASNLQDEELCGGLWRLVLAQRWMERLKTVA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPRPPMASVVRLPPGSVIAPMPPIIHAPRINVVPMPPSAPPIMAPRPPPMIVPTAFVPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSKKTTTYYESINEVCNQYLKSYEKKPLVII-----QILG--W----SQRLMRYYKTVD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TKPIPPKLIEPKKSEDSKNLQRPRIPDSPKPIKNSQPEAPKPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain PCC 7120 is a synonym of sequence_revision 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:BA000019; F
ce: strain PCC
                                                                                          7.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EPPKPWERVPKKPS
                                                                                                                                                                                                                                                                                                                          T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.;
                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                Score 88.5; pr
Pred. No. 23;
28; Mismatches
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Pred. No. 3;
                                                                                                                                                                                          NID: g3413913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VVRKIPKVIETPKIVKPQKTEDIKTLES
     -GPVLSDRRLCLA--LDEPQLCNGHMGGASRR 1148
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                                                                                                                                                                                        PIDN:BAA32321.1;
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                                                                                                        Length
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                                                                                                                                                                                                                                                                                            cDNA libraries
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                                                                       63;
                                                                                                                                                                                       PID: 93413914
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                                                                    Gaps
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                                                                       12;
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                                                                A; Title: Complementation of fission yeast cdc2(ts) and A; Reference number: S12008; MUID:91006056; PMID:2120044
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A;Residues: 1-227,'A',229-479 <JIM>
A;Cross-references: EMBL:X57495; NI
                                 A; Molecule type: mRNA
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                                                  A; Accession: S12008
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A;Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; R;Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M. EMBO J. 9, 3565-3571, 1990
                                                                                                                                                            protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog C;Species: Drosophila melanogaster C;Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_C;Accession: A32290; S12008 R;Edgar, B.A.; 0'Farrell, P.H. Cell 57, 177-187, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JQ0532
OP protein
                                                                                                               Cell 57, 177-187, 1989
A;Title: Genetic control of cell division patterns in the A;Reference number: A32290; MUID:89195217; PMID:2702688
                                                           A; Molecule type: mRNA
A; Residues: 1-479 <EDG>
                                                                                                    A; Accession: A32290
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A; Residues: 1-753 <DIN>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The nucleotide sequence of the genomic RNA of A;Reference number: JQ0532; MUID:90218040; PMID:2324710 A;Accession: JQ0532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: JQ0532
R;Ding, S.; Keese, P.; Gibbs, A.
J. Gen. Virl. 71, 925-931, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                              587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 LLLLLLPYGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPDVFHDCQPSSPTSHVVGYRRLLGSGISLPFKLAFW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLSTQPPSSPQTSSSPPPPSPRTDASGIQTPLASPPSKRKEKSLPHPSHQ----PPSHSK 475
                                                                                                                                                                                                                                                                                                                                                                              PRKL
                                                                                                                                                                                                                                                                                                                                                                                                                    PODL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNLRRHSALPLLLPIHPTKTTQPHPAVPQP--TAGPTPHPPPTKKIPLHPPKSQERHPSP 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNFSR----CLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VESGAWAYLSPLVLRKELESLVENEGSEV-----LALPELPSAHPIIFWNLLWYFQRL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLVALKPWITRQNFSRCLELQCQ-PDSSTLPPPW-SPRPLEA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -WRVHSQ-IPQRVVWPG----PVPASLSLALLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 88; DB
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                           25-Apr-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 753;
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NID: 97706; PIDN: CAA40732.1;

PID: 97707

cdc25(ts)

mutants

identifies

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C;Genetics:
A;Gene: FlyBase:stg
A;Cross:references: FlyBase:FBgn0003525
Search completed: May 27, 2003, 18:27:59 Job time: 22 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match. 7.0%; Score 87.5; D. Best Local Similarity 22.9%; Pred. No. 8.2; Matches 56; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and
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9/Active site: Cys (phosphocysteine intermediate) #status predicted
                                                                                                                243 VTISH 247
                                                                                                                                                                231 LLVEH 235
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Y192_HUMAN
ATF5_MOUSE
SGCA_MOUSE
EPC_HUMAN
DIA1_HUMAN
IF4G_RABIT
CEFD_STRCL
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KPC1_COCHE
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-!- SUBUNIT: Homodimer (1soform 2)!- SUBCELLULAR LOCATION: Type I membrane protein (1soform 1); secreted (1soform 2)!- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here) and 2/soluble; are produced by alternative splicing.	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  MEDLINE-20343011; PubMed-10881197; Savvides S.N., Boone T., Karplus P.A.; "Flt3 ligand structure and unexpected commonalities of helical bundles and cystine knots."; Nat. Struct. Biol. 7:486-491(2000).  -i- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.	33:2795-2801(1994). E FROM N.A., AND ALTERN. E-96032581; PubMed-75669. S.D., Stocking K., Daviss. C S.; C S.; cural analysis of human included the second se	(2) SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-94235842; PubMed-8180375; Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Lyman S.D., James L., Johnson L., Beckmann M.P., McKenna H.J.; Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.; "Cloning of the human homologue of the murine fitt3 ligand: a growth "cloning of the human homologue of the murine fitt3 ligand: a growth factor for early hematopoletic progenitor cells.";	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLIND-94195428; PubMed-8145851;  Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.;  Hazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,  Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,  Buda G., Martina N., Peterson D., Menon S., Shanafelt A.,  Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G.,  Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;  Tigand for FLT3/FLK2 receptor tyrosine kinase regulates growth of  haematopoietic stem cells and is encoded by variant RNAs.";  Nature 368:643-648(1994).	01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3T). 11gand) (Flt3T). FLT3TG. Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelecia; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID-9606;	RESULT 1

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There are no restrictions ng as its content is in

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RESULT 2
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Matches 235
                                                                                  FL3L_MOUSE STANDARD; PRT; 232 AA. PA9772; 064085; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) SL cytokine precursor (Fms-related tyrosine k ligand) (Fl13L).
SEQUENCE FROM N.A. MEDLINE-94195428;
                                           Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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CONFLICT
SEQUENCE
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EMBL: U29874; AAA90949.1; --
EMBL: U29874; AAA90950.1; --
EMBL: U29874; AAA90950.1; --
EMBL: U29874; AAA90950.1; --
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                                                                              OR FLT3L
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 PubMed=8145851;
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Rodentia;
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G -> A (IN REF. 1).
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EXTRACELLULAR (POTENTIAL).
                                           Craniata; Ver
Sciurognathi;
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73B95BF693B4CECF CRC64;
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                                          Vertebrata;
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EMBL; U29875; AAA90951.1; --
EMBL; U29875; AAA90952.1; --
EMBL; S76459; AAB33069.1; --
EMBL; S76461; AAB33070.1; --
EMBL; S76461; AAB33071.1; --
EMBL; S76461; AAB33071.1; --
EMBL; U44024; AAA93307.1; --
EMBL; U44024; AAA93306.1; --
EMBL; U44024; AAB9L; --
EMBL; U44024; AAA93306.1; --
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Mattei M.-G., Rosnet O., Birnbaum D., Hannum C.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULAT:
FACTORS AND INTERPRITUTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
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modified and this statement is not removed. Usage by and for con-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTORS AND INTERLEUKINS.
SUBUNIT: Homodiner (soluble isoform) (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Two soluble isoforms are also produced by alternative splicing. One of isoform 3/E6, is biologically active, while the other, isof 4/E6Delta16, is inactive.

ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2/5H, and 4/E6Delta16; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                            Pro; IPR004213; Flt. PF02947; flt3_lig;
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11:1165-1172(1995).
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                  SEQUENCE FROM N.A.

MEDLINE-86306657; PubMed-3018124;

Davison A.J., Scott J.E.;

"The complete DNA sequence of varicella-zoster virus.";

J. Gen. Virol. 67:1759-1816(1986).

-!- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPE
ACTIVATION OF ALPHA GENES.
                                                                                                                                                                                            Varicella-zoster virus (strain Dumas)
Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10338;
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GBR2.HUMAN STANDAKU;
GBR2.HUMAN STANDAKU;
GPR2.HUMAN STANDAKU;
GPR2.HUMAN STANDAKU;
GPR2.HUMAN STANDAKU;
GPR2.HUMAN STANDAKU;
GPPR2.HUMAN STANDAKU;
GPPR2.H
                                                                                                                                                                                                                                                                                    "Cloning and characterization of a novel human with high affinity for GABA and low affinity fo Submitted (NOV-1998) to the EMBL/GenBank/DDBJ d
                                                                                                             TISSUE-Hippocampus;
Borowsky B., Laz T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20193514; PubMed=10727622; Clark J.A., Mezey E., Lam A.S., Bonner "Distribution of the GABA(B) receptor sprain Res. 860:41-52(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GABA(B) receptor.";
Nature 396:679-682(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White J.H., Wise A., Main M.J., Gree Barnes A.A., Emson P., Foord S.M., Pare Barnes A.A., Emson P., Foord S.M., Pare Barnes A.A., Pare Bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2A).
TISSUE-Cerebellum;
MEDLINE-99087321; PubMed-9872316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005051; Herpes_UL46.
Pfam; PF03387; Herpes_UL46; 1.
Transcription regulation; Trans-acting
SEQUENCE 661 AA; 74272 MM; C5CA77A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; x04370; CAA27895.1;
C27342; TNBE12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLWRLVLAQRWMERLKTVAGSKMQGLLERVN----TEIHFVTKCAFQP---PPSCLRFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parker
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                                                                          3., Laz T.,
(JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISOFORM 2A).
McCrea K., Watson
                                                                                                                                                                                                     (ISOFORM 2A).
                                                                          Gerald
to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.4%;
26.6%;
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                                                                                                                  <u>က</u>
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C5CA77A16D365379 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Green A., Fraser N.J.,
M., Marshall F.H.;
for the formation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ή.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2в
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND
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                                                                                                                                                                                                                                                                                    an GABA-B receptor for baclofen."; J databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disney G.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287
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                                                                                                                                                                                                                                                                                                                                                                        subtype
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SEQUENCE

FROM

N.A.

the

EMBL/GenBank/DDBJ

databases

restrictions

for

commercia.

50

a collaboration

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WEDLINE-20237752; PubMed-10773016; Sullivan R., Chateauneuf A., Coulombe N., Kolakowski L.F. Jr., Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K., Abramovitz M., O'Neill G.P., Ng G.Y.K., "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B)) receptor 4 sith truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional receptor.";
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                                                                                                                                                                                    <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonner T.I., O'Neill G.P.;
"Identification of a GABAB receptor subunit, gb2, required for functional GABAB receptor activity.";
J. Biol. Chem. 274:7607-7610(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of a novel G-protein-coupled receptor GPR 51 resembling receptors expressed predominantly in nervous tissues and mapped proximal to the hereditary sensory neuropathy type 1 locus on chromosome 9.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99175124; PubMed-10075644;
Ng G.Y.K., Clark J., Coulombe N., Ethler N., Hebert T.E., Sullivan R.,
Kargman S., Chateauneuf A., Tsukamoto N., McDonald T., Whiting P.,
Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin S.C., Russek S.J., Farb D.H.;
"Molecular identification of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ng G.Y.K., McDonald T
Chateauneuf A., Coulor
O'Neill G.P., Liu Q.,
"Cloning of a novel G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression GABABR1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rla-R2 INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99263199; PubMed-10328880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 56:288-295(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fetal brain;
MEDLINE=99189236; P
ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN CEREBRAL CORTEX, THALAMUS, HIPPOCRAMPUS, FRONTAL, OCCIPITAL AND TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLOM, FOLLOWED BY CORPUS CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, ANYGDALA AND MEDULLA.

WEAKLY EXPRESSED IN HEART, TESTIS AND SELETAL MUSCLE.

DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION MEDITATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MOREOVER COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HETERODIMER OF IS EFFECTIVE ON ITS OWN
                                                                                                                                                                                                                                                      PREREQUISITE FOR PLASMA MEMBRANE.
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nald T., Bonnert T., Rigb
Coulombe N., Kargman S.,
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Caskey T., Evans
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Matches 26
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EMBL; AF056085; AAC6328.1
EMBL; AF095723; AAC63383.1
EMBL; AF095724; AAC633834.1
EMBL; AF095784; AAD30389.1
EMBL; AF095784; AAD303336.1
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DOMAIN
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Pfam; PF01094; ANF_Teceptor; 1.

PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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HGNC:4507; GPR51
 26; Conservative
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ipr000337; GPCR_Mgr.
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AAC63328.1;
AAC63384.1;
AAC63384.1;
AAD30389.1;
AAD30336.1;
AAD45867.1;
AAD45867.1;
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COTLED COIL (POTENTIAL).
N-LINKED (GLCNAC...) (PC
 Score 89.5; E
Pred. No. 6.4;
2; Mismatches
                                                                                    /FTId-VAR_010149.

S -> R (IN REF. 5

P -> R (IN REF. 5

G -> E (IN REF. 3
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            DB
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                                                                                                                                                                                                                         CARBOHYD
SEQUENCE
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DOMAIN
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by modified
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FEBS Lett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sakamoto A. Ono K., Abe M., Jasmin G., Eki T., Murakami Masaki T., Toyo-oka T., Hanaoka F.;
"Both hypertrophic and dilated cardiomyopathies are caus of the same gene, delte-sarcoglycan, in hamster: an anin disrupted dystrophin-associated glycoprotein complex."; proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
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STRAIN-F1B; TISSUE-Skeletal muscle;
MEDLINE-95278335; PubMed-7758576;
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Mammalia; Eutheria;
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EMBL; U21677;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberds S.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX. SUBCELLULAR LOCATION: Type I membrane protein. Sar
                  GGLWRL----
                                                             TTRQRLLLLI--
                                                                                              TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC
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                                                                                                                                       h 7.2%;
Similarity 23.4%;
71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pean Bioinformatics Institute. The non-profit institutions as long and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
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41, Last annotation update)
precursor (Alpha-SG) (Adhalin)
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Rodentia;
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POTENTIAL.
ALPHA-SARCOGLYCAN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                       Score 89; DB
Pred. No. 2.6;
% Mismatches
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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Sciurognathi; Muridae; Cricetinae;
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RESULT 6
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              В
RX MEDLINE-20057165; PubMed-10591208;
RX MEDLINE-20057165; PubMed-10591208;
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clagg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clagg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clagg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clagg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clagg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
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RA Clagg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clagg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Martyn I.D., Mashreghl-Mohammadi M., Matthews L.H., McCann O.T.,
RA McClay J., McLaren S., McMurray A.A., Milnes S.A., Mortimore B.J.C.T.,
RA McClay J., McLaren S., McMurray A.A., Milnes S.A., Mortimore B.J.,
RA McClay J., McLaren S., McMurray A.A., Milnes S.A., Mortimore B.J.,
RA Williams L., Hulbard T., Bentley B.R., Sulston J.E., Swann R.M.,
RA Williams L., Hulbard T., Bentley D.R., Salter M.N., Willey D.L.,
RA Williams L., Hulbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Salter T., Asakawa S., Kudoh J.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Phan S., Jaking F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Phan S., Jaking R., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Mang Q., Wang Y., Wan
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01-NOV-1997
15-JUN-2002
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"Mammalian splicing factor SF3al20 represents
SURP family of proteins and is homologous to
factor PRP21p of Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-96079958; PubMed-7489498;
Kraemer A., Mulhauser F., Wersig C.,
"Mammalian splicing factor SF3al20 r.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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SF3A1 OR SAP114.
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Q15459;
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Metazoa; Primates; C
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(Rel.
(Rel.
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35, Last sequence update)
41, Last annotation update)
subunit 1 (Spliceosome asso
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Catarrhini; Hominidae;
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ts a new member
o the essential
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Homo.
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                                                                                                                                                                                                                                                                                                                                                                                     Hall C.,
                                                                    H. F.,
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Query Match
Best Local
        Matches
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EMBL; AC004997; A
HSSP; Q15843
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DOMAIN
                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO00061; Surp.
InterPro; IPRO00626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
Pfam; PF01805; Surp; 2.
SMART; SM00213; UBO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
Hinds K., Kemp K., Latrellle P., Layman D., Ozersky P., Rohlfing T.,
Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
MCDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
Wilkinson P. Rodenfeich A. Hartman K.
                                                                                       SEQUENCE
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DOMAIN
                                                                                                                                                                                              REPEAT
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The DNA sequence of human chromosome 22.";
Nature 402:489-495(1999).
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Tilahun Y., Wright H.;
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                                                                                                                                                                                                                                                                                                                         ROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF US NRNP TO BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA, SEQUENCE INDEPENDENT BINDING OF SF3A/SE3B COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSENTIAL, IT MAY ANCHOR UZ SNRNP TO THE PRE-MRNA. MAY ALSO B INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.

SUBUNIT: COMPONENT OF SPLICING FACTOR SF3B WHICH IS COMPOSED THREE SUBUNITS; SF3AJ/SAP61, SF3AJ/SAP62, SF3AJ/SAP114. SF3A ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TEORM THE UZ SMALL NUCLEAR RIBONUCLEOPROTEINS COMPLEX (UZ SNRN THE UZ SMALL NUCLEAR RIBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTS WITH SF3A3.
SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    605595; -
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  67; Conserv
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                                                                                       793
      Conservative
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7; AAC23435.1;
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                                                                                                                                                                                                                                                                                                                     UBIQUITIN_2; 1.
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208
793
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                                                                                       98886
                     7.2%;
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  34;
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POLY-PRO.
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POLY-GLN.
  Pred. No. 5.8; Mismatches
                                                                                 POLY-PRO.
POLY-PRO.
; 7259F1EC4577305C CRC64;
                                           Score
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SURP MOTIF 2.
UBIQUITIN-LIKE.
                        No.
                 DB
5.8;
    79;
                                         Length 793;
    Indels
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Gaps
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4 LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63

MGD;

MGI:104875; Ltb rPro; IPR001368;

Ltbr.

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TNR3_MOUSE
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                         EMBL; U29173; EMBL; L38423; EMBL; U30798; HSSP; O14763;
                                                                                                                                                                                                                                              sequence trap and chromosomal mapping.,
Genomics 30:312-319(1995).
-!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member
                                                                                      entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                 Honjo T.;
"The murine lymphotoxin-beta receptor cDNA:
"sequence trap and chromosomal mapping.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CVB; TISSUE-Lung;
MEDLINE-96072804; PubMed-7594541;
Force W.R., Walter B.N., Hession
                                                                                                                                            between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                  Nakamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                  "Mouse lymphotoxin-beta receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Browning J.L., Ware C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTBR OR TNFRSF3 OR TNFCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNR3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250284;
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96163885; PubMed=8586432;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Lymphotoxin-beta receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                             (By similarity).
SUBUNIT: Self-associates (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPPAPAPDEYLV-
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                                                                                                                                                                                                                                                                                                                                                                                                      155:5280-5288(1995)
                                                                                                                                                                                                                                                                                                                                                  Tashiro
                                     AAB00846.1;
AAA81334.1;
                                                               AAA68964.1; -.
                          100G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                Nazarea M., Nakano T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular genetics, ligand binding
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                                                                                                                         There are no rest
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thi; Muridae;
                                                                                                    http://www.isb-sib.ch/announce/
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Best Local
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[2]
SEQUENCE FROM N.A.
MEDLINE-91006056; PubMed-2120044;
Jimenez J., Alphey L., Nurse P., G
                                                                                             SEQUENCE FROM N.A.

MEDLINE-89195217; PubMed-2702688;
Edgar B.A., O'Farrell P.H.;

"Genetic control of cell division
Cell 57:177-187(1989).
                                                                                                                                                                                                         STG OR CDC25 OR CG1395.

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                          MPIP_DROME STANDARD; PRT; 479 AA. P20483; O9VAL9; O1-FEB-1991 (Rel. 17, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) M-phase inducer phosphatase (EC 3.1.3.48) (St)
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CARBOHYD
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NCBI_TaxID=7227;
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REPEAT
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SMART; SM00208; TNFR; 3.

PROSITE; PS00652; TNFR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
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BY SIMILARITY
BY 
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Pred. No. 3
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EXTRACELLULAR (POTENTIAL).
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               Glover D.M.
t cdc2ts and
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                 cdc25ts mutants
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                                                                                                                                                                                                                                Brachycera;
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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams N.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., RA Adams N.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Brandon R.C., Rogers Y. H.C., Blazej R.G., Champo M., Pfeiffer B.D., Ray Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen I.X., Ray Brandon R.C., Rogers Y. H.C., Blazej R.G., Champo M., Pfeiffer B.D., Ray Bank R.M., Basal A., Baxendale J., Bayaktaroglu L., Beasley E.M., Ray Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ray Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier R.A., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ray Borson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., Ray Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier R., Chandra I., Berson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., Ray Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier S., M.R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Ray Bortova D., Bortell J.H., Gu Z., Guan P., Barris M., Glasser K., Rosler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K., Rosler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K., Ray Bortova D., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Kambulla M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Kambulla M., Kalush F., Karpen G.H., McDerson D.A., Mechanson D.A., Mechanson D.A., Mesharty C., Morris J., Moshrefi A., Musiken D.L., Mary D.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ray Mullians S.M., My M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ray Borten G., Stapleton M., Skupski M.P., Smith T., Shen H., She
                                                                                              EMBL; M24909; AAA28916.1; --
EMBL; X57495; CAAA40732.1; --
EMBL; AE003768; AA4756885.1;
PIR; A32290; A32290.
PIR; S12008; S12008.
                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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string.";
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SIMILARITY: BELONGS TO THE MPI
SIMILARITY: CONTAINS I RHODANES
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FlyBase; FBgn0003525; stg.
InterPro; IPR000751; MPI\_Phosphatase.
InterPro; IPR000763; Rhodanese-like.
Pfam; PF00581; Rhodanese; 1.
PRINTS; PR00716; MPIPHPHTASE.

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Best Loc
Matches
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ACT_SITE
CONFLICT
SEQUENCE
                   between
                                                                                                                                                                                      STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-94173920; PubMed-8127887; Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbacid "Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of Ptk-3, a receptor expressed in proliferative zones the developing brain.";
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00450
Cell division;
                                                                                                                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ý Match
Local Similarity
hes 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
European
                                                                                      TYPOSIDE Phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECTIFICITY: VARIOUS EMBRYONIC AND ADULT
PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HII
SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS
                                                                                                                                           C. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).
FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS RECOGNITION (BY SIMILARITY).
CATALYTIC ACTUSTY: ATP + a protein tyrosine - ADP
                                                             SIMILARITY:
SIMILARITY:
             SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                        OR EDDR1 OR PTK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTISH 247
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479 AA
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      Bioinformatics
                                                  SUBFAMILY.
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19 430
79. 379
28 228
3 AA; 54094 1
                                                          : CONTAINS
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BY SIMILARITY.
A -> T (IN REF. 1).
W; 68483F3A285962CC (
       Institute.
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4; Mismatches
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Pred. No. 4.4;
                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                        TYR FAMILY OF PROTEIN
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                                                                                         D ADULT TISSUES; ALSO AIN; HIPPOCAMPAL NEURONS DOMAINS OF TYR-PROTEIN
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                                                         KINASES.
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      restrictions
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               a collaboration
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    outstation -
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Best Local S
Matches 38
DDRI_MOUSE STANDARD; PRT; 911 AA. (203146; 203146; 203146; 201-0CT-1994 (Rel. 30, Created) 01-0CT-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epithelial discoidin domain receptor 1 precursor Epithelial discoidin kinase CAK) (Cell adhesion kina
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Pfam; PF00754; F5_F8_type_C; 1.

ProDom; PD000001; Euk_pkinase;

SMART; SM00231; FA58C; 1.

SMART; SM00231; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; Glya
Phosphorylation; Transmembrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; P$00239; RECEPTOR TYR_KIN_II; PROSITE; P$501285; FA58C_1; 1.

PROSITE; PS01286; FA58C_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
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                                                                                                                471 NRPGPREPPPYQEPRPRGTPTHSAPCVPNGSALLL
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                                                                                                                                                                        -----PLLLLELLPVGLLLLAAAWCLHWQR----TRRR-----
                                                                                                                                                      ILIGCLVAIILLLLIIALML----WRLHWRRLLSKAERRVLEEELTVHLSVPGDTILIN
                                                                                                                                                                                             PWLLFSEISFISDV-VNDSSDTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTA
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                                                                                                                                                                                                                                               Similarity
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32
510
789
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391
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GLY/PRO-RICH
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F5/8 TYPE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE
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SIMILARITY
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; Glycoprotein; Signature; Signatur; ATP-binding.
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                                                                                                                                                                                                                                                        1;
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      rsor (EC
kinase)
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      (Tyrosine kinase
                2.7.1.112
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SMART; SM00231; FA58C; 1.

SMART; SM00219; TyrKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_MTP; FALSE
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS01236; FA58C_1; 1.

PROSITE; PS01286; FA58C_2; 1.

Transferase; Tyrosine-protein kinase; Glyco
                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coexpressed in breast tumor cell lines Oncogene 12:1469-1477(1996).
                                           Alternative
                                                      Phosphorylation;
                                                                                                                                                                                                                                                                                                  HSSP;
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                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perez J.L., Jing S.Q., Wong T.W.;
"Identification of two isoforms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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InterPro; IPR000421; FA58_C.
InterPro; IPR002011; RTKinaseII.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6; TISSUE-Embryonic MEDLINE-93096484; PubMed-1281307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 766-822 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                               BL; L57509; AAB05209.1;
CAA40516.1;
R; S30502; S30502
SP; P00523; ZPTK.
D; MGI:99216; Ddr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK
ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
ABSENCE OF A 37 RESIDUES SECHENT.
TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN VAR
DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR SUBFAMILY.
SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPING EMBRYO AND ADULT EPITHELIAL CELLS.
SIMILARITY: BELONGS TO THE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                 PF00069; pkinase; 1.

PF00754; F5_F8_type_C; 1.

m; PD000001; Euk_pkinase;
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                                                      Transmembrane;
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POTENTIAL.

EPITHELIAL DISCOIDIN DOMAIN RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                     Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain;
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tor; ATP-binding;
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Best Local S
Matches 38
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE-96009859; PubMed-7546742; Koerschen H.G., Illing M., Seifert R., Se Gotzes S., Colville C., Mueller F., Dose Kaupp U.B., Molday R.S.; "A 240 kDa protein represents the complet nucleotide-gated channel from rod photore Neuron 15:627-636(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNG4_BOVIN STANDARD; PRT; 1394 AA.

Q28181; Q28082; Q03861;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

240 kDa protein of rod photoreceptor CNG-channel [Contains: Glutamic acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4

(CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel modulatory subunit)].
MEDLINE=96198098; PubMed=8626431;
Biel M., Zong X., Ludwig A., Sautter A.,
"Molecular cloning and expression of the
cyclic nucleotide-gated cation channel.";
J. Biol. Chem. 271:6349-6355(1996).
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DOMAIN
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NCBI_TaxID=9913;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
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CYTOPLASMIC
F5/8 TYPE C
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de M., Molday L.,
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Best Local Similarity
Matches 35; Conser
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EMBL; X94707; CAA64367.1; --
EMBL; M61185; AAA30536.1; --
InterPro; IPR000630; M+Channel_nlg.
InterPro; IPR000595; cNMP_binding.
Pfam; PF00027; cNMP_binding; 1.
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Ionic channel; Ion transport; CAMP-b
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Submitted (XXX-1991) to the
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SEQUENCE OF 1-590 FROM
                                                                                                                                                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: FORMS FUNCTIONAL HETEROOLIGOMERIC CHANNELS WITH CNG3.
SUBCELLULAR LOCATION: Integral membrane protect.
ALTERNATIVE PRODUCTS: 3 ISOFORMS; CNG4C (SHOWN HERE), CNG4D
AND CNG4E: ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR
THE MOST FREQUENT FORM (CNG4D:CNG4C:CNG4E = 20:2:1) IN TESTIS.
TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
FAMILY.
                                                                                                                                                                                                                                                                           989
1073
1094
1081
1141
                                                                                                                                                            1067
515
522
341
454
482
499
572
                                 Conservative
                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       786
800
819
844
                                          7.0%;
                                                                                 155064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
                                                                             R -> Q (IN REF. 2 AND
A -> T (IN REF. 3).
VPATEEHPELQVEDADADS -:
R (IN REF. 3).
S -> A (IN REF. 2).
R -> A (IN REF. 2).
D -> E (IN REF. 2).
A -> AA (IN REF. 2).
A -> AA (IN REF. 2).
                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsujimoto M., Khorana H.G., ]
e EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                             MISSING
K -> E (
                                                                                                                                                                                                                                                                                                                                         H4 (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
                                            Score 86.5;
Pred. No. 18
                             Pred. No. 18;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLICING:
GLUTAMIC ACID-RICH PROTEIN.
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4.
                                                                                                                                                                                                REEEEDEEEEQD
                                                                                                                                                                                                                                                               CAMP (POTENTIAL).
                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
H6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                           H3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
H2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
H1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cAMP-binding; Transmembrane;
                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                            E (IN REF.
                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
                                                                                                                                                                                                                       (GLCNAC. . .) (POTENTIAL)
(IN ISOFORM CNG4E).
(IN ISOFORM CNG4D).
                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                        DB
                                                                                                                                                                                             -> MRAGOKGRC (IN REF. 2)
                                                      Ļ,
                                                                                                                                                                                 AND
                                                      Length 1394;
                                                                                                                                                           -> GSFQMSPFEALQECEALK
                                                                                 CRC64;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ichikawa A:;
                              41;
                            Gaps
                             5.
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-- QETSEQLVALKPWITRQNFSRCL 154

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ATF5_HUMAN
ID ATF5_H
AC Q9Y2D1
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                                                                                                                                                                                                                      Query Match
Best Local S
Matches 21
ATF5_HUMAN
Q9Y2D1; Q9UNQ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the cellular compartment.";

J. Cell Biol. 109:3493-3501(1989).

J. Cell Biol. 109:3493-3501(1989).

-I FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE), THE COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.

-!- PIM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                 Glycoprotein; Sulfation; Hydroxylation
DOMAIN 228 340 PRO-RICH.
260 295 POLY-PRO.
SEQUENCE 485 AA; 50436 MW; A522164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-f. Nagariensis / HK10; MEDLINE-90094551; PubMed-2689458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V1-MUV-1994 (Rel. 19, Last sequence up
01-0CT-1996 (Rel. 34, Last annotation
Sulfated surface glycoprotein 185 (SS)
Volvoy cartors
                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carter1: molecular structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Volvox carteri.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VOLCA
                                                                                                                                                                                                                                                                                                                                              PIR; A33647; A33647.
                                                                                                                                                                                                                                                                                                                                                                EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGP_VOLCA
P21997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Volvocaceae; Volvox.
                                                                                            309 PVPPPPSPPSVL
                                                                                                                                                                                     160 PDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGE 219
                                                                                                                         220 QVPPVPSPQDLL 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRT
                                                                                                                                                                                                                                      Similarity
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                    Score 86; DB Pred. No. 5.9; 3; Mismatches
                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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ation update)
5 (SSG 185).
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                282 AA
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                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                   Length 485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outstation
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Best Local
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human Cdc34 and Rad6B ubiquitin-conjugating enzymes target repr
"Human Cdc34 and Rad6B ubiquitin-conjugating enzymes target repr
of cyclic AMP-induced transcription for proteolysis.";
Mol. Cell. Biol. 19:5001-5013(1999).
-1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)
(CONSENSUS: 5'GTGACGT(A/C)(A/G).3'), A SEQUENCE PRESENT IN M
VIRAL AND CELLULAR PROMOTERS.
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cyclic-AMP-dependent transcription factor ATF-
transcription factor 5) (Transcription factor
                                                                                                                                                                                                                                                                                     DNA_BIND
                                                                                                                                                                                                                                                                                                                                                       Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20558615; PubMed-11087824; White J.H., McIllhinney R.A.J., Wise A., Emson P.C., Billinton A., Warshall F.H.; "The GABAB receptor interacts directly wi
                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 606398; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:790; ATF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF101388; AAD28370.
TRANSFAC; T04877; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 161-282 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [nterPro;
  179
                                                                                144 WIT-RONESRCLELQCOPDSSTLPPPWSPRP--LEATA----
                                           66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                      WMTERVDFTALLPLEPPLPPGTLPQP-SPTPPDLEAMASLLKKELEQMEDFFLDAPPLPP.124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF305687; AAG22558.1;
AB021663; BAA78477.2;
                                                                                                                                                                                                                                                                                                                                                                                            SM00338; BRLZ; 1.
E; PS00036; BZIP_BASIC;
                                                                                                                                  . Similarity
38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRBB2 and ATFx.";
atl. Acad. Sci. U.S.A. 97:13967-13972(2000)
                                                                                                                                                                                                                                                                                                              BZIP_BAS
___on regulation; L
e family.
123
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                                                                                                                                                                                                                  186
210
236
161
282
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                                                                                                                                Conservative
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Primates;
                                                                                                                                                                                                                     30674 MW;
                                                                                                                                                  6.8%;
                                                                                                                                                                                                                                                                                                                                                                     SIC; 1.
DNA-binding;
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POLY-PRO.
BASIC MOTIF.
LEUCINE-ZIPPER (PROB
LLA -> RHE (IN REF.
LLA -> DDBZF907CA0215A0 C
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                                                                                                                           Score 85; DB Pred. No. 3.9; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
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                                                                                                                                                                                                                                                                                                                                                                       Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There
                                                                                                                                              DB 3.9;
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                                                                                                                             38;
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                                                                                                                                                                       Length 282
                                                                                                                                                                                                                  CRC64;
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                                                                                                                             44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repressors
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STRUCTURE 6:63-73(1998).

STRUCTURE 6:63-73(1998).

STRUCTURE 6:63-73(1998).

STRUCTURE FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGE FROM MILK AND HELPS NERBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGE IN THE MILK IS BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE RESULTANT FCRN-IGE COMPLEXES ARE TRANSCYTOSED ACROSS THE INTESTINAL EPITHELIUM AND IGE IS RELEASED FROM FCRN INTO BLOOD CONSISTED FLOIDS (BY SIMILARITY).

-ISSUE FLUIDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FCGN_RAT P13599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95059482; PubMed=7969498; Burmeister W.P., Huber A.H., Bjor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simister N.E., Mostov K.E., "Cloning and expression of the neonatal rat intestinal Fc major histocompattbility complex class I antigen homolog." Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Epithelium;
MEDLINE-90315866; PubMed-2534798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGG receptor FCRN receptor) (IGG FC FCGRT OR FCRN.
                                                                                                                                                                                                                                                                                                                                                            Vaughn D.E., Bjor)
                                                                                                                                                                                                                                                                                                                                                                                          x-ray Crystallography (2.2 angsth
MEDLINE=98154319; PubMed=9493268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simister N.E., Mostov K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990
01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Crystal structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "An Fc receptor structurally related Nature 337:184-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89097257; PubMed-2911353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
IGG receptor FCRN large subunit P51 precursor (FCRN) (Neonatal receptor) (IGG FC fragment receptor transporter, alpha chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 372:379-383(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 VPPVPSP
                                                                                                                        LIKE HETERODIMER.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSPPPLPPPPLPPAPSLPLSLPSTDLPQPPVLDTLDLLAIYCRNEAGQEEVGMPPLPPPQ
                                                                                                                                                                                                                                                                                                                                                            Bjorkman
basis of p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            pH-dependent antibody binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     f., Bjorkman P.C
complex of rat
                                                                                                                                                                                                                                                                                                                                                                                                          ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ៥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neonatal Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I antigens.";
                                                                                                                                                                                                                                                                                                                                                            by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor with
                                                                                                                                                                                                                                                                                                                                                            neonatal
                                                                                      a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor,
                                                                                                                                                                                                         P14 WHICH
                                                                                                                                                                                                                                       BLOOD OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
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restrictions EMBL

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RESULT 15
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR001039; MHC_I.
Pfam; PF00047; Ig; 1.
Pfam; PF00129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                            Q61329;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-fetoprotein enhancer binding protein (A'
(AT-binding transcription factor 1).
                                                                                                                                                                                                                                                                            _MOUSE
ABF1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X14323; CAA3250;
EMBL, M35495; AAA41611
PIR; S02117; S02117.
PIR; A37374; A37374.
PDB; 1FRT; 14-FEB-95.
PDB; 3FRU; 10-JUN-98.
SEQUENCE FROM N.A.
STRAIN-BALB,MK X ICR; TISSUE-Brain;
MEDLINE-96104902; PubMed-8654949;
Ido A., Miura Y., Watanabe M., Saka:
Hashimoto T., Morinaga T., Nishi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS
                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                             308
                                                                                                                                                                                                                                                                                                                                                                                        196 LLLLA---AAWCLHWQRTRRRTPR------PGEQVPPVPSPQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                         254
                                                                                                                                                                                                                                                                                                                                                                                                                                                         154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 RKESEFLLTSCP-----ERLLGHLERGRONLEWKEPPSMRLKARPGNSGSSVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                        LLLYVVAIAGGVLLWNRMRSGLPAPWLSLSGDDSGDLLPGGNLPPEAEPQ 357
                                                                                                                                                                                                                                                                                                                                                                                                                    GDGSFHAWSLLEVKRGDEHHYQCQVEHEGLAQPLT---VDLDSPARSSVPVVGIIL---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------TCAAFSFYPPELKFRFLRNGLA-------SGSGNCSTGPN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTEIHFVTKCA---FQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRC---- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELSDYLLQDYPYTVASNLQDEELCGGLWRLYLAQRWME----RLKTVAGSKMQGLLERV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 22.:
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00290; IG_MHC; 1.
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23
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                                                                                                                                                (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAA32503.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LEL-----QCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA41611.1;
                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . . .
    M., Sakai
Nishi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGG RECEPTOR FCRN LARGE
EXTRACELLULAR ALPHA-1
EXTRACELLULAR ALPHA-3
EXTRACELLULAR ALPHA-3
CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. ..) (PO
N-LINKED (GLCNAC. ..) (PO
N-LINKED (GLCNAC. ..) (PO
N-BA8BF2873A698BB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                             Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR FCRN LARGE
                                                                                                                                                                                                                                                                            3726 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 366;
    Inoue
moki T.
                                                                                                                                                                                            (AT
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                  ۲.,
                                                                                                                                                                                          motif-binding
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                   Miki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) (POTENTIAL).
) (POTENTIAL).
                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                               Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT P51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal;
                                                                                                                                                                                            factor)
                                                                                                             Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
 TRANSFAC; 103881;

MGD; MGI:9948; Attb1.

InterPro; IPR001356; Homeobox.

InterPro; IPR000822; Znf_C2H2.

InterPro; IPR003604; Znf_U1.

Pfam; PF00046; homeobox; 4.

Pfam; PF00096; zf-C2H2; 20.

PF000m; PD000010; Homeobox; 4.

SMART; SM00359; HOX; 4.

SMART; SM00359; ADF_C2H2; 22.

SMART; SM00351; ZnF_C2H2; 22.
                                                                                                                                                                      DNA-binding;

ZN_FING

                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of the cDNA encoding the mouse ATBF1 transcription factor."; Gene 168:227-231(1996).
-!- FUNCTION: Transcriptional activator that binds to the AT-rich cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00027; HÖMEOBOX_1; 2.
PROSITE; PS00071; HOMEOBOX_2; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D26046; BAA05046.1; -.
HSSP; P20263; 10CP.
TRANSFAC; T03881; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Transcriptional activator that binds to the sequence of the enhancer element of the AFP gene. -!- SUBCELLULAR LOCATION: Nuclear. -!- SIMILARITY: CONTAINS 4 HOMEOBOX DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription
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1734
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2405
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1009
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1113
11256
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3011
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2308
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                                           POLY-PRO.
POLY-ALA.
POLY-PRO.
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POLY-ALA.
POLY-ALA.
POLY-GLN.
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C2H2-TYPE
C2H2-TYPE
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C2H2-TYPE.
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C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2H2-TYPE (ATYPICAL).
C2H2-TYPE (DEGENERATE).
C2H2-TYPE (ATYPICAL).
                                                                                           POLY-GLN
                                                                                                                                                                                                                                                                       C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                      C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ATYPICAL)
                                                                                                                                                                                                                                                                                      (ATYPICAL).
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FT DOMAIN 3620 3623 POLY-PRO. FT DOMAIN 3659 3662 POLY-SER. SEQUENCE 3726 AA; 406567 MW; 915ACBE588A72C98 CRC64;  QUETY MATCH Best Local Similarity 21.68; Pred. No. 80; Matches 53; Conservative 29; Mismatches 70; Indels 93; Gaps 12;  QV 29 DCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86;

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                         Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein -
                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                             840
835
602.5
578
112.5
1104.5
100.5
98.5
98.5
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                                                                                                                                                                                                                                        Match
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  May 27, 2003, 18:26:11 ; Search time 34 Seconds (without alignments)
1424.149 Million cell updates/sec
                                72.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-994-468-6
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                                                                                                                                                                                                                                                                                                                                                          sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_mammal:*
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                                                                                                                                                                                                                                      DB
 Q9DWH8
Q9C5T0
Q17889
Q8VD70
                                                                                 Q9GKD9
Q61104
Q8VCH4
Q9LGG8
Q9GY11
Q9GY33
                                                        Q8VIM6
Q9N753
                                                                                                                                                                             Q9MZVO
Q9MZU9
Q9GKEO
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        O9mzv0 canis famil
O9mzu9 felis silve
O9gke0 bos taurus
O8wnw1 bos taurus
O8vnw1 bos taurus
O61104 mus musculu
O8vch4 mus musculu
O9vch4 mus musculu
O9lg98 oryza sativ
O9lg98 oryza sativ
O9gy11 leishmania
O9gy31 sishmania
O9gy31 sishmania
O9gy33 leishmania
O9vim6 mus musculu
O9n753 leishmania
O9dwh8 rat cytomeg
O9c5t0 arabidopsis
O17889 caenorhabdi
                                                                                                                                                                                                                                  Description
Q8vd70 mus musculu
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8 8 5 5	85	85	85.5	86	86	86	86	86.5	87	89	87.5	87.5	88	88	88	88.5	88.5	88.5	88.5	88.5	89.5	90.5	90.5	90.5	92	92.5	92.5
0 0 0 0	o	•		•					7.0	7.0	7.0	7.0	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.2	7.3	7.3	7.3	7.4	7.4	7.4
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## ALIGNMENTS

180	121	Qy
120	61 ASNLODDELCGAMKLYLAQRWMXRKLKIYAGSKMQGLLERVNTEIHFVTKCAFQPPSCL 	B 2
60	1 MIVLAPAWSPTASLLLLLLLSPGLRGTPDCSFSHSPISSTFAVTIRKLSDYLLQDYPVTV	
60	Qy 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60	_
Gaps	Query Match 72.1%; Score 895.5; DB 6; Length 294; Best Local Similarity 77.1%; Pred. No. 3.5e-80; Matches 182; Conservative 12; Mismatches 35; Indels 7; Ga	
	SQ SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;	
~	RT degree of similarity to the human and mouse homologue but uniquely RT long cytoplasmic domain.";	
	-	
	RD SHOTTENON N N	
	NCBI_TaxID=9615;	
	OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
		_
	Fit3 ligand.	
	01-JUN-2002	
	7	
	RESULT :	

B 5

181

APQPP-LLLLLLPVGLLLLAAAWCLHW-QRTRRRTPRPGEQVPPVPS-----

-pop

RFVQTNISHLLQDTSQQLAALKPWITRRNFSGCLELQCQPDSSTLVPPRSPGALEATALP 180

APQAPRLLLLLLPVALLLMSTAWCLHWRRRRRRRSPYPGEQRTLRPSERSHLPED 236

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121

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RESULT
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Best Local S
Matches 178
                                                                                                                                                                                                                                                                                                          Q9GKE0
Q9GKE0;
01-MAR-2001 (TIEMBLIFEL 16, C
01-MAR-2001 (TIEMBLIFEL 16, L
01-DEC-2001 (TIEMBLIFEL 19, L
Flt3 ligand isoform-1.
SEQUENCE FROM N.A.

MEDLINE-20570936; PubMed-11120823;

Mwanqi W., Brown W.C., Palmer G.H.;

"Identification of fetal liver tyrosine kinase 3 (Flt3) ligand

required for receptor binding and function using naturally occu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9MZU9;
Q9MZU9;
01-OCT-2000
                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Cetartiodactyla; Rum
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Seq. 11:163-166(2000).
EMBL; AF155149; AAF87089.1; -
EMBL; FOR004213; F1t3_11g,
Pfam; PF02947; F1t3_11g; 1,
SEQUENCE 291 AA; 32459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fells silvestr1s catus (Cat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Bumanlia; Eutheria; Carnivora; Fissipedia; Felidae;

NCBi_TaxID-9685;
                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of canine and feline flt3 ligand reveals high degree of similarity to the human and mouse homologue but uniquely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20358731; PubMed-10902925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APQPP-LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFVQTNISHLLQDTSEQLAALKPWITRRNFSGCLELQCQPDSSTPLPPRSPRALEATALP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASNLODDELCGPFWHLVLAQRWMGRLKAVAGSQNQSLLEAVNTEIHFVTLCAFQPLPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
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178; Conserv
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 4.3e-80;
9; Mismatches 33
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                                                                                                                                                                                                                               ca; Vertebrata;
Ruminantia; Per
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Best Local
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01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-2000) to the EMBL/GenBank/DDBJ EMBL; AB051841; BAB79634.1; TITERFORMELS; FITS_11g; TIPRO04A13; FITS_11g; TIPRO4A13; FITS_11g; TIPROMERTED; TIPROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hikono H., Momotani E.; "Cloning of a cDNA for bovine flt3 ligand. Submitted (NOV-2000) to the EMBL/GenBank/I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Cetartiodactyla; Rur
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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  181
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                               TAPOPP---LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQ 220
                                                                                                                                                                                                                                                    LRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAP
                                                                                                                                                                                        VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMOGLLERVNTEIHFVTKCAFQPPPSC
PGPQSPLLLLLLLLLPVALLLLATAWCLCRWRRRRTRYPGER
                                                                                                                                                                  VASNLQDDKLCGAFWRLVLAQRWMGRLKTVAGSEMEKLLEDVNTEIHFVTSCAFQPLPSC
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                                                                               LRFVQANISHLLQDTHQQLEALKPWITHRNFSRCLELQCQPDSPTLLPPRSPGALGATSL
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75.9%;
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76.38;
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21,
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                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                             Score 835; DB
Pred. No. 3.2e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
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Pred. No. 1e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ta; Vertebrata; Euteleostomi;
Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292
                                                                                                                                                                                                                                                                                                                                                                 DB 6;
.2e-74;
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RESULT
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Best Local
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SEQUENCE FROM N.A.

MEDLINE=20570936; PubMed=11120823;

MWang1 W., Brown W.C., Palmer G.H.;

MWang1 W., Brown W.C., Palmer tyrosine kinase

"Identification of fetal liver tyrosine kinase
"Identification of fetal liver tyrosine kinase
                                                                                                                                                         McClanahan T., Culpepper J., Campt
Mattson J., Tsai S., Luh J., Guime
Birnbaum D., Hannum C.;
"Flt3 ligand: expression, genomic
                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Mus musculus (Mouse).
Merazoa; Chordata;
Merazoa; Rodentia;
                       InterPro; IPR004213; Flt3_lig.
InterPro; IPR001230; Prenyl_site
Pfam; PF02947; flt3_lig; 1.
                                                                               forms and processing.";
Submitted (DEC-1995) to the I
EMBL; U44024; AAA93305.1; -.
MGD; MGI:95560; Flt31.
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Fit3 ligand, T169 form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q61104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute:
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel 16, 01-MAR-2001 (TrEMBLrel 16, 01-DEC-2001 (TrEMBLrel 19, Flt3 ligand isoform-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GKD9
                                                                                                                                                                                                                                               EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF288986; AAF99323.1; -
Pro; IPR004213; F1t3_11g.
PF02947; f1t3_11g; 1.
NCE 274 AA; 30372 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 60.1%;
Similarity 69.6%;
56; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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PRENYLATION; UNKNOWN_1
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21,
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Last sequence update)
Last annotation updat
                                                                                                                     EMBL/GenBank/DDBJ
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Pred. No. 1.8e
12; Mismatches
                                                                                                                                                                                                   Campbell
Guimares
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                             organization,
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                                                                                                                                                                                                   W. C
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                                                                                                                                                                                                   Wagner J.
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M.-G., Rosnet
                                                                                                                                                                                                                                                                                                                        Euteleostomí;
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                                                                                                                                                                                                                                                                                                     Murinae;
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RESULT OBVCH4
ID Q8
ID Q8
AC Q8
DT 011
DT 011
DT 011
DT 011
DT 011
RR S1
RR NC NC
RR SE
RC TIL
RR SE
RC TIL
RR SE
RC TIL
RR ST
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         Q9LGG8 PRELIMINARY; PRT; 579 AA.

Q9LGG8;

Q9LGG8;

Q1-CCT-2000 (TrEMBLrel. 15, Created)

T 01-CCT-2000 (TrEMBLrel. 15, Last sequence update)

T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Putative extensin-like protein.

P0406H10.6 OR OJI174_D05.5.

N P0406H10.6 VITICALED.

C Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

C Spermatophyta; Magnoliophyta; Liliopsida; Poales; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 120
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Best Local Similarity
Matches 122; Conserv
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted DEC-2001) to the EMBL/GenBank/DDBJ EMBL; BC019601; AAH19801.1; -. InterPro; IPR004213; Flt3_119. Pfam; PF02947; flt3_119; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Submitted (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
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hes 120;
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                                                                                                                                                                                                                                                                                                                                                                                LREVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKWQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                                                                                                                                                                                                                                                                                                           LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LREVOTNISHLIKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDRVSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTVLAPAWSP-TTYLLLLLLLSSGLSGTODCSFOHSPISSDFAVKIRELSDYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18986 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.5%; Sc
72.6%; Pr
tive 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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Pred. No. 1.5e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 578; DB 11;
Pred. No. 3.7e-49;
4; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5B4CA47D9724EFF2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5e-51
                                   Embryophyta; Tracheophyta;
a; Poales; Poaceae;
                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                           TPPPCCPQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 54
                    Murphy L., Quail M., Harris D., Rajandream M., Oliver K.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AL390114; CAC02038.2; -.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR0001611; LRR.
InterPro; IPR002965; Prich_extensn.
Pfam; PF00560; LRR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01582; KV33CHANNEL.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00370; LRR; 5.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SEQUENCE 579 AA; 62607 MW; 04457E18
SMART; SM00181; ESF; 1.
                                                                                                                      SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                      Q9GY11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Oryza sativa nipponbare(GA3) genomic clone:011174_D05.";
                                                                                                                                                                                                                      01-OCT-2001
01-JUN-2002
                                                                                                                                                                                                                                                          Q9GY11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP002524; BAB07956.1; --
EMBL; AP003118; BAB33013.1; --
InterPro; IPR001511; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic clone:P0406H10.";
           PRINTS; PR01217; PRICHEXTENSN
                                                                                                                                                         NCBI_TaxID=5664;
                                                                                                                                                                    eishmania major.
Sukaryota; Euglenozoa;
                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                         Probable surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00560; LRR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002965; P_rich_extensn.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                  392
                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                                                                                                                 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILLINTGLS------SCLPPEVGM-LREVTVF------DVSFNRLAGPLPSA 282
                                                                                                                                                                                                                                                                                                                                                       TAPOPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                             NI--SRLLQETSEQLVALKPWITRQNFSR----CLELQCQPDSSTLPPPWSPRPLEATAP
                                                                                                                                                                                                                                                                                                                                                                                                                          VAGMRKVEQL-DVAHNLLTGAIPQAVCELPRLKNFTFAYNFFTGEPPSCAHAVPRYGDRR 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLAQRWMERLKTVAGSKMQGLLERVNTETHFVTKCAFQ-----PPPSCLRFV-----QT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                            NCLPNRPAQRTLRQCAAF-----FARPPVNCAAFQCKPFVPALPPPSPPPP--SPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                   (TrEMBLiel.) (TrEMBLiel.) (TrEMBLiel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIPPONBARE;
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.1%; Score 112.5; DB 23.7%; Pred. No. 0.013;
                                                                                                                                                                    Kinetoplastida;
                                                                                                                                                                                                                     16,
18,
21,
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Last annotation update)
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                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                               ----SPPPPSTSPPPSP 411
                                                                                                                                                                                                                                                                    899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA, chromosome 1,
                                                                                                                                                                   Trypanosomatidae;
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                                                                                                        X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                 databases
                                                                                                        Ivens
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                                                                                                       Α.,
                                                                                                                                                                   Leishmania.
                                                                                                        Barrell
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RESULT
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Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                      InterPro: IPR002965;
Pfam; PF00560; LRR; 7
PRINTS: PR01217; PRIC
SMART; SM00181; EGF;
SEQUENCE 648 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9GY33;
01-MAR-2001
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000561;
InterPro; IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AL390114; CAC02017.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     Murphy L., Quail M., Oliver K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probable surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9GY33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002
                                                 289
                                                                         161
                                                                                                  230.
                                                                                                                           119
                                                                                                                                                   195
                                                                                                                                                                                                    149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 DSSTEPPPWSPR-----PLEATAPTAPQPP-----LLLLLLLPVGLL--LLAAAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 CLREVQ---TNISRLLQ------ETSEQLVALKP-WITRQNFSRCLELQCQP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 LPPEWSSMPNLQTLQVRRLKLSGT-----LPADWS-SLKSLSNVVLEDMPIT----
           11
                                                                                                                                                                           64
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                                                                                                                                                                                                                                                     Local Similarity
les 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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                                                                                            ALRELTLDGTNLSGTLPPQWSAMASVISLNLEGTEVSGTLPPEWISMSRL-QTLNLRRTK
                                                                                                                                                                                                                       LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
                                                                                                                        CLREVQ---TNISRLLQ-----
                                                                                                                                                                                                 LPPEWSSMPNLNAVELKRLKLSGT------LPADWS-SLKSLSNVVLEDMPIT----
                                              VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMKKLTQLLLTDTLLSGTLPAEW 345
                                                                       DSSTLPPPWSPR----PLEATAPTAPQPP----
                                                                                                                                                  -----GL----LPPEW
                                                                                                                                                                         LQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP-----S 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMRKLTQLLLTDTLLSGTLPAEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALRFLTLDGTNLSGTLPPQWSAMASVISLNLEGTEVSGTLPPKWISMSRL-QTLNLRRTK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------GL----LPPEW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP-----S 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                          IPR002965;
0560; LRR; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 16, C
(TrEMBLrel. 18, I
2 (TrEMBLrel. 21, I
urface antigen p2.
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                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                PRICHEXTENSN
                                                                                                                                                                                                                                                                                                      68470 MW;
                                                                                                                                                                                                                                                                                                                                                                     LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70725 MW;
                                                                                                                                                                                                                                                              8.3%; Score 102.5; D
26.6%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                 EGF-like.
                                                                                                                                                                                                                                                                                                                                                      P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 104.5; DB 26.6%; Pred. No. 0.093;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                    8EB78AC101E01286 CRC64;
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEB3ECAABC490C94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rajandream
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                                                                                                                      ETSEQLVALKP-WITRQNFSRCLELQCQP
                                                                                                                                                -GSLERIQQLVLRKLKVTGPLPPQWSPMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GSLERIQQLVLRKLKLTGPLPPQWSPMK 229
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                                                                       -LLLLLLPVGLL--LLAAAW
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Best Local S
Matches 70
Submitted (AUG-2001) to the EMI
EMBL; AL390114; CAB98658.2; -.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
Pfam; PF00560; LRR; 3.
SMART; SM00370; LRR; 3.
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01-OCT-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                    Murphy L., Quail M., Oliver K.;
                                                                                                                                                                                                                                             STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probable surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9N753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9N753
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Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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01-MAR-2002
01-JUN-2002
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EMBL; AF375593; AAL35321.1; ...
MGD; MGI:2153816; Strc.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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Verpy E., Masmoudi S., Zwaenepoel I., Leibovici M., H.
Del Castillo I., Nouaille S., Blanchard S., Laine S.,
Moreno F., Mueller R.F., Petit C.;
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                                                                                                                                                                                                                                                                                                                                                            Kinetoplastida; Trypanosomatidae;
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Last annotation update)
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Last sequence up
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Pred. No. 0.74;
5; Mismatches
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Best Local Similarity
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Virus Res. 69:119-130(2000).
EMBL; AF232689; AAF99111.1; -.
SEQUENCE 1240 AA; 125612 MW;
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MEDLINE-20473137; F
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MEDLINE-20366325;
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Betaherpesvirinae; Muromegalovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEDLINE-20366325; PubMed-10906222;
Vink C., Beuken E., Bruggeman C.A.;
Complete DNA sequence of the rat cytomegalovirus
, Virol. 74:7656-7665(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --WLLRTAQRPPLSPPPRQRPPRTSLT---
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                                                                                                                                                                                                                                                                                                                                                                            Similarity
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., Beuken E., Bruggeman C.A.,
rus R89 is a highly conserved
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23.8%; Pre
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Last sequence update)
Last annotation updat
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Q9C5T0; Q9C5T0; 01-JUN-2001 01-JUN-2001

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Best Local S
Matches 34
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Pfam; PP01657; DUF26; 2.

Pfam; PP00069; pkinase; 1.

ProDom; pD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00229; TyrKC; 1.

PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS001107; PROTEIN_KINASE_DOM; 1.

ATP-binding; Kinase; Transferase
SEQUENCE 658 AA; 72991 MW; DCF9CF5F1
                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
F54F12.1 protein.
"Gename sequence of the nematode investigating biology."; Science 282:2012-2018(1988). EMBL; Z8I%48; CABO4464.1; -.
                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID-6239;
                                                    none;
                                                              SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                     Submitted (NOV-1996)
                                                                                                                    Barlow
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                      017889
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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1 Similarity 25.8%;
34; Conservative 1
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Ser_thr_pkinase.
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                                                                                                  the EMBL/GenBank/DDBJ databases
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Last sequence upon Last annotation
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Pred. No. 1.1;
16; Mismatches
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Search completed: May Job time : 38 secs
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InterPro; IPR000242; TYI_PP.
Pfam; PF00102; Y_phosphatase; 1.
SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                SEQUENCE
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 1
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
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                                                                            LPVGLLLLAA----AWCLHWQRTRRRTPRPGEQVPPVPSP
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                                                                                                                            ALKPWITRQNFSRCLELQCQPDSSTL---PPPWSPRPLEATAPTAP---
                                                                                                                                                       MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL---
                                                                                                   ALRPQPTTSDPTAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII
                                                                                                                                                                                                             Similarity
38; Conserv
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nilarity 23.6%;
Conservative 3
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            18:28:40
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2.6;
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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EP627487-A. 07-DEC-1994

Domain Domain

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(IMMV ) IMMUNEX CORP
                       17-JUN-1997;
                                                                      23-DEC-1998
                                                                                             WO9857655-A1
                                                                                                                    Homo sapiens
                                                                                                                                                   Antigen-specific peripheral immune tolerance; flt3-ligand; immunogenic; autoimmune disease; organ transplantation; fo
                                                                                                                                                                                        Human flt3-ligand
                                                                                                                                                                                                                 25-MAR-1999
                                                                                                                                                                                                                                         AAW67769
                                                                                                                                                                                                                                                             AAW67769 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                             Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or therapeutic molecule, respectively. The polypeptide is capable of binding the fit3 receptor and is: a) amino acids 28-x of murine fit3 ligand (fit3-L), where x is an amino acid between 163-231; b) amino acids 28-y of human fit3-L, where y is an amino acid between 160-235; and c) a polypeptide that has at least 90% identity to the polypeptides. of either (a) or (b). The method ameliorates the effects of autoimmune diseases, food allergies or organ or tissue rejection following transplantation. Administration of fit3-L allows lower doses of antigens to be used in vivo for mucosally administered antigens. The present sequence represents human fit3-L.
                                                                                                                                                                                       multiple myeloma;
                                                                                                                                                                                                              cancer; dendritic cell; immune response; autoimmunity;
myelodysplasia; aplastic anemia; HIV infection; lympho
                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                               Full length wild type human flt-3 protein.
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WO200001823-A2

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel soluble filt3 ligand (filt3.1) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (this sequence) or mature (AAK99720) filt3.1 Cpolypeptides. The filt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic propentior cells. The filt3-L protein can be used to induce cellular cexpansion (especially in vivo) or differentiation, e.g. the contract of hematopoietic, natural killer (NK) or dendritic cells, especially in the cexpansion (especially in vivo) or differentiation, e.g. the growth factors such as interlegikins, colony stimulating compresence of growth factors such as interlegikins, colony stimulating contents or protein kinases. The protein fan be used to treat an immune content (e.g. allergy, autoimmunity or immunosuppression). The protein disorder (e.g. allergy, autoimmunity or immunosuppression). The protein constrain cancer (e.g. allergy, autoimmunity or immunosuppression). The protein constrain cancer (e.g. allergy, autoimmunity or immunosuppression) testicular or contents and cancer (e.g. allergy, autoimmunity or immunosuppression) testicular or lenkemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 235
 Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine; immunotherapy; therapy; tumour; cancer; melanoma; glioma; lymphoma; autoimmune disease; infection; gene therapy. Homo sapiens.
                                                                                            Human Flt-3
                                                                                                                    14-MAY-2001
                                                                                                                                                                           AAB20192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                    APOPPLLILLLIPVGLLLLAAAWCLHWORTRRRTPRPGEOVPPVPSPODLLLVEH 235
                                                                                                                                                                                                                                                                                                                                             ASNIODEELCGGIWRLVLAQRWMERLKTVAGSKMQGLLERVNTETHFVTKCAFQPPPSCL 120
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235; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 soluble flt3 ligand polypeptide used in cellular expansion, response stimulation or treatment of pathological conditions as amino acid substitutions at positions 8, 84, 118 or 122
                                                                                                                                                                          standard; Protein;
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Pred. No. 5e-109;
0; Mismatches, 3 0;
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121

61 61

RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT

180

MTVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV

Query Match Best Local S Matches 235

Similarity

100.0%;

Score 1242; DB 2 Pred. No. 5e-109; Mismatches

22; 0;

Indels Length

0

Gaps

0

60 60 Conservative

0;

Sequence

AA;

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The present sequence is that of human Fms-like tyrosine kinase (Fit-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Fit-3 cadministering in vivo, into a tissue of a vertebrate, a Fit-3 controlled encoding polynucleotide, and I or more antigen or a Fit-3 controlled may encode the present full-length human Fit-3 controlled may encode the present full-length human Fit-3 controlled may encode the present full-length human Fit-3 controlled polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, controlled to the cells of the vertebrate in vivo, and a prophylactically contine cells of the vertebrate in vivo, and a prophylactically contines or cytokines is produced in vivo, and a prophylactically compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, considered the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B contous other examples of these diseases are given in the contous other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic compositions comprising Fit-3 ligand encoding polynucleotide and one or more antigen, or cytokine encodi polynucleotides, useful for suppressing tumour growth and autoimmune diseases (e.g. rheumatoid arthritis)
                             specification.
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 132-133; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-123319,
N-PSDB; AAF30310.
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Peptide
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206..235
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27..182
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27..235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane_domain
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RESULT 5
ABBO1129
ABBO1129
ABBO1129
ACC ABBO
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XX DT 10-S
XX DE Humm
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                                                                                                                                                                                                                                                                                                             The invention relates to treating an individual at risk for or suffering from infection with a pathogenic or opportunising organism. The method convolves administering a combination of two to dive agents comprising:

(a) dendritic cell mobilisation factor;
(b) dendritic cell mobilisation agent; (c) dendritic cell maturation agent; (c) dendritic cell activation agent; (d) ricell enhancing factor;
(c) are activated, antigen-specific T cells. The methods are useful for treating an individual at risk for or suffering from infection with a ceg. M. tuberculosis, yeast, fungi (e,g) c albicans or protozoa (e.g. M. tuberculosis), yeast, fungi (e,g) c albicans or protozoa (e.g. method is useful for treating an individual suffering from immunosuppression by cenhancing a lymphocyte-mediated immune response. In particular, the herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, of cell leukemia or T cell lymphoma. The activated antigen-presenting represents a human fitsl polypeptide fragment, that can be used as a central cell mobilisation factor.
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30-OCT-2001; 2001WO-US44834.

R 02-NOV-2000; 2000US-245721P.

X (IMMY) IMMUNEX CORP.

I Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE IT Thomas EK;

X WPT; 2002-500114/53.

PT Treating an individual suffering from infection, e.g. inflammation, of chickenox or AIDS, by administering a combination of denoritic cell pri antigen-specific T cells - antigen-specific T cells - antigen-specific T cells - antigen-specific T cells - affering an infering from antigen-specific T cells - affering antigen-specific T cells - affering antigen-specific T cells - affering the combination of the cell of the combination of the combination of the combination of the cell of the combination of the cell of the combination of the cell 
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Best Local Similarity
                                                                                                                                                        Matches 235;
                                                                                                                                                                                                                                                                                         Sequence
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MTVLAPAMSPTTYLLLLLLLSGLSGTQDCSFQHSPISSBFAVKIRELSDYLLQDYBYTV 60
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                                                                                                                                                                                                                                                                                  235 AA;
                                                                                                                                              Conservative
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                                                                                                                                       Score 1242; I
Pred., No. 5e-1
0; Mismatches
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RESULT 6
AAR66175
             C A cDNA library from the human stromal cell line 298V4B, in pME18S, was screened with an 800 bp fragment derived from mouse clone T11B. This fragment encompasses the coding region conserved between two mouse clones, T11B and T110. Approx. 20 positive clones were selected and partially sequenced. Two clones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to show homology to T110 until the stop codon, although to a lesser degree, for an overall homology of 66%. Clones T11B and S109 do not show homology to each other or to the other clones after mouse residue 163 (human residue 160). An additiona mouse clone designated MBB has a 29 AA insert at the junction between the common and divergent portions of the mouse ligand.
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07-JUL-1993
16-JUL-1993
13-AUG-1993
24-AUG-1993
19-NOV-1993
                                                                                                                                                                                 Claim 11; Page 76-77; 90pp; English.
                                                                                                                                                                                                    New ligand for the Flt3 tyrosine kinase receptor - and rel nucleic acid, vectors, host cells and antibodies, useful f treating abnormal cell physiology and proliferation, e.g. also for diagnosis and drug screening
                                                                                                                                                                                                                                                                  WPI; 1995-006787/01.
N-PSDB; AAQ79642.
                                                                                                                                                                                                                                                                                                                           (INRM )
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                                                                                                                                                                                                                                                                                                     Birnbaum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flt3 ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human S86/S109 Flt3 ligand peptide sequence.
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93US-0089263.
93US-0092549.
93US-0166340.
93US-0112391.
93US-0155111.
93US-0162413.
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Best Local
                            The
       The present sequence (Flt-3 ligand). The
                                                                                                              Immunogenic compositions comprising fit 3 ligand encoding polynucleotide and one or more antigen, or cytckine encoding polynucleotides, useful for suppressing tumour growth and autoimmune diseases (e.g. rheumatoid arthritis)
                                                                                                                                                                                                                                                                                                       Hermanson
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immunotherapy; therapy; tumour; cancer; melanoma; glioma;
lymphoma; autoimmune disease; infection; gene therapy.
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DB; AAF30312.
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                                               Page 137-138; 149pp; English.
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27..235
/label= Mature_protein
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/label-_Extracellular_domain
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is that of human Fms-like tyrosine invention is directed to enhancing
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02-JUL-1998; 25-JUN-1999;

98US-0109100 99WO-US14296 13-JAN-2000 WO200001823-A2

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(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections;

(b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
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Best Local
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                                                                                                                                                                                                                           Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell;
                                                                                                                                      Homo sapiens.
Synthetic.
                                                                                                                                                                                cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein.
                                                                                                                                                                                                                                                                                                             Human flt-3 mutein L-3H.
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No. 1.8e-108;
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Human; flt-3 receptor agonist.

KW bone marrow reconstitution; haematopoietic ceil stimulation; cancer; where the constitution; haematological disease; immune deficiency; drug-induced myelosuppression; renal dialysis; gene therapy; infection; congenital metabolic disease; neurological disease; therapy; for dendritic cell production.

KM dendritic cell production.

KM dendritic cell production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides CC which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L. CC polypeptides. This sequence represents an example of the novel flt3-CC polypeptides. This sequence represents an example of the novel flt3-CC polypeptides and comprises the L-3H mutant polypeptide. The flt3-L; protein CC binds cell surface tyrosine kinase receptors and regulate growth and CC differentiation, e.g. in hematopoletic progenitor cells. The flt3-L; protein CC differentiation, e.g. in hematopoletic, natural killer (NK) on dendritic CC cells, especially in the presence of growth factors such as interleukins, CC colony stimulating factors or protein kinases. The protein can also CC modulate, augment or enhance a patient's immune response and can be used CC immunosuppression). The protein may be used to treat an immune disorder (e.g. allergy, autoimmunity or condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, CC small cell lung, testicular or ovarian cancer, lymphoma, multiple completed and contact of the condition or acute leukemia.
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(IMMV) IMMUNEX CORP.

(X Graddis TJ, McGrew JT;

(X WPI; 2000-182115/16.

(X MV Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions or contains amino acid substitutions at positions 8, 84, 118 or 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Page 79-80; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.5%; Score.1124; DB.21; Length 21234 tlarity 100.0%; Pred. No. 5.9e 98; Conservative 0; Mismatches 0; Indels 0; Gaps
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RESULT 10
AAY69720
ID AAY69
XX
AC AAY69
XX
DT O5-JU
XX
DE Matur

AAY69720 standard;

Protein; 209

A

Mature wild 05-JUL-2000

type human flt-3

밁 Qy

147

RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH

206

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180

RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH

В Š

181

WORTERETPERFGEQVPPVPSPQDLLLVEH

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                                 Q_{\underline{Y}}
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                                                                                                     QY
                                                                                                                                                                                                                             This sequence represents a rearranged human flt-3 receptor agonists of CC the invention. The agonists have a modified flt-3 ligand amino acid consequence. The agonists are used to stimulate production of haematopoietic cells in vivo (e.g. in a subject about to donate blood) or for ex vivo expansion for subsequent transplantation, e.g. to reconstitute bone conserved after chemotherapy, disease etc., or to treat haematological confections, burns or renal dialysis. Optionally ex vivo expanded cells are transduced with a gene therapy vector for treating e.g. congenital confections, immune deficiency, neurological disease, cancer and confections. The agonists can also be used in the treatment of tumours, infections and autoimmune disease, when administered optionally with an antiquen. The agonist can also be used in the production of dendritic cells for use as an immunising adjuvant for treatment disorders including acquired immune deficiency syndrome. Compared with native ligands, the converse have better stimulatory activity, reduced side effects and/or better physical properties such as solubility, stability or refold efficiency. When used together with other stimulatory agents, the
                                                                                                                                                Ouery Match
Best Local Similarity
Matches 209; Conserv
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Staten N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rearranged filt-3 receptor agonists and nucleic acids encoding them used to stimulate production of haematopoletic and dendritic cells, for treatment of haematological diseases, bone marrow reconstitutic and in gene therapy
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                                                                                                                                                                                                                           Sequence
61
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                                                                                           TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                 KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
                                                                      TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
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                                                                                                                                                  Conservative
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                                                                                                                                                                89.7%; Score 1114; DB 19; 100.0%; Pred. No. 5.1e-97;
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PR, Woulfe SL;
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                                                                                                                                                                                                                                                                                              Query Match
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Matches 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3.L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 89-90; 90pp; English.
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RONFSRCLELQCOPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH KTVAGSKMQGLLERVNTEIHFVTECAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 멍 ğ

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Query Match Best Local ! Matches

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89.4%;

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The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides CC which exhibits increased or decreased biological activity relative to CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L CC polypeptides. This sequence represents an example of the novel flt3 CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein CC binds cell surface tyrosine kinase receptors and regulate growth and CC differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, CC colony stimulating factors or protein kinases. The protein can also comodulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, conditions a newship and concer, lymphoma, multiple
Sequence
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Pred. No. 1.2e-96;
1; Mismatches (
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27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86

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RESULT 13
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The invention relates to novel soluble fit3 ligand (fit3-L) polypeptides C which exhibits increased or decreased biological activity relative to the full length wild type (AAX69719) or mature (AAX69720) fit3-L CC polypeptides. This sequence represents an example of the novel fit-3 CC ligands and comprises the L26F mutant polypeptide. The fit3-L protein CC binds cell surface tyrosine kinase receptors and regulate growth and CC differentiation of hematopoietic progenitor cells. The fit3-L protein can be used to induce cellular expansion (especially in vivo) or CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, cc colony stimulating factors or protein kihases. The protein can also CC modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, cc small cell lung, testicular or ovarian cancer, lymphoma, multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 82-83; 90pp; English.
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RESULT 14
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             The invention relates to novel soluble flt3 ligand (flt3-L) polypepti which exhibits increased or decreased biological activity relative to the full length wild type (AAY6979) or mature (AAY6979) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L26F mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and
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Mutant soluble flt3 ligand polypeptide used immune response stimulation or treatment of

amino acid substitutions

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positions

in cellular expansion, pathological condition

conditions or 122 -မ္မ

WPI; 2000-182115/16

02-JUL-1998;

98US-0109100 99WO-US14296

25-JUN-1999;

WO200001823-A2 Synthetic Homo sapiens

(IMMV ) IMMUNEX CORP

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Best Local S
Matches 208
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                                                                                                                                                                                                                                                                                                    cell surface tyrosine kinase receptor, hematopoletic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cencer; dendritic cell; immune response; autoimmuntly; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
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Best Local Similarity 99.5%;
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides. This sequence represents an example of the novel fit-3 ligands and comprises the H87 mutant polypeptide. The fit3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoletic progenitor cells. The fit3-L protein can be used to induce cellular expansion (especially in viyo) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoliminity or immune condition e.g. myelodysplasia, applastic anemia. HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                              207 WQRTRRRTDRPGEQVPPVPSPQDLLLVEH 235
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/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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            US-09-904-536-10
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US-09-904-536-12
US-09-904-536-17
US-09-904-536-17
US-09-904-536-17
US-09-904-536-13
US-09-904-536-13
US-09-904-536-13
US-09-904-536-13
US-09-904-536-13
US-09-904-536-13
US-09-904-536-16
US-10-03-33554-16
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Sequence 1/ Appli
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1680,	SD				9
e 104,			7.0	87.5	8
104,	9 US-09-991-496-104			87.5	37
Sequence 57, Appl	_		7.0	87.5	6
8			7.0	87.5	5
Sequence 20, Appl	10 US-09-907-372-20		7.0	87.5	4
e 6,			7.0	87.5	ω
20,			7.0	87.5	2
Sequence 30, Appl			7.1	88	ï
Sequence 2, Appl1	9 US-10-109-324-2	1257	7.1	88.5	ö
Sequence 47, Appl			7.2	89.5	9
о 4-			7.2	89.5	8
31	9 US-10-300-616-31		7.2	89.5	27
•	٦,		7.2	89.5	8
26,			7.2	89.5	55
е 5			7.4	91.5	24
8 A	9 US:-09-863-818A-8		7.4	91.5	3
509,	9 US-09-866-050A-509		7.4	91.5	22
2, 7	US-09-899-471-		7.4	91.5	2
Sequence 19, Appl	10 US-09-904-536-19	137	40.8	506.5	õ

## ALIGNMENTS

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/669,692

FILING DATE: 24-JUN-1996

APPLICATION NUMBER: US/08/162,407

FILING DATE: December 3, 1993

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

APPLICATION NUMBER: 08/106,946

FILING DATE: May 24, 1993

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floopy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
FILING DATE: 13-Mar-2002
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lýman, Stewart D.

Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
REFERENCE/DOCKET NUMBER: 2813-C TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                           NAME: Malaska, Stephen L. REGISTRATION NUMBER: 32,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Washington COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
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; ORGANISM: Homo sapiens
US-09-448-378-1
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US-09-448-378-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 235
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                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2836-D
CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS;
LENGTH: 235 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                               181 APOPPILLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                               181 APOPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVDSPQDLLLVEH 235
                                                                                                                         121 REVQTNISRLLQETSEQLVALKPWITRONFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
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                                                                                                          REVOTNISRLLQETSEQLVALKEWITRQNESRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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Pred. No. 1.4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           Matches 235;
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      181
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                                                                                                                                                           1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                                                                                                                                                                                                                                      1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
                        APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                    RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
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MEDIUM TYPE: Floppy disk
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                                                                              RFVQTNISRLLQETSEQLVALKPWITRQNESRCLELQCQPDSSTLPPPWSPRPLEATAPT
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TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lyman, Stewart D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 235 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/983,806 FILING DATE: 25-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 233-0644 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Washington COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1242; ilarity 100.0%; Pred. No. 1.. Conservative 0; Mismatches
LPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-1
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                                                                                                                                                   Query Match 90.5%; Score 1124; | Best Local Similarity 100.0%; Pred. No. 3e Matches 211; Conservative 0; Mismatches
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGREW, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 235; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02
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                RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPW 144
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                                                                     SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME 61
                                                                                                            SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME 84
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Pred. No. 1.4e-101;
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US-09-904-536-18
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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Best Local Similarity
Matches 209; Conserv
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SEQ ID NO 18
LENGTH: 209
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                                                    SOFTWARE: PatentIn Ver. SEQ ID NO 9
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APPLICANT: McGrew, Jeffrey T.
TITLE ONVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
                                                                                                          PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02
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PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
                   LENGTH: 20
TYPE: PRT
                                                                                          NUMBER OF SEQ ID NOS: 20
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TYPE: PRT
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ORGANISM: Homo sapiens
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PRIOR FILING DATE: 1999-07-1
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 209
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US-09-904-536-12
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                                                                  Sequence 14, Application US/09904536 Patent No. US200201111475A1 GENERAL INFORMATION:
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            APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/904,536
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APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260,0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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ORGANISM: Homo sapiens
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey I
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SOFTWARE: PatentIn Ver.
SEQ ID NO 14
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CURRENT FILING DATE: 2001-07-16
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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PRIOR APPLICATION NUMBER: PRIOR,
PRIOR FILING DATE: 1999-07-02
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TYPE: PRT
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tes 208; Conserv
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WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
               WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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                                                                            RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
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Pred. No. 5e-90;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-15
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US-09-904-536-11
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PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                          Matches 208;
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                                                                                                                                             Query Match
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Best Local Similarity
Matches 208; Conserv
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CURRENT FILING DATE: 2001-07-16
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 02260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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TYPE: PRT
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                                 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 60
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Pred. No. 7.4e-90;
D; Mismatches 1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-13
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US-09-904-536-13
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                                  SOFTWARE: PatentIn Ver.
SEQ ID NO 8
LENGTH: 209
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGREW, Jeffrey T.
APPLICANT: MCGREW, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
                                                                                                                                                                                                                                                                                Sequence 8, Application US/09904536 Patent No. US20020111475A1
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Best Local Similarity
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                                                                                      FILE REFERENCE: 03260.0028

CURRENT APPLICATION NUMBER: US/09/904,536

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100

PRIOR FILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 20
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
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ORGANISM: Homo sapiens
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Pred. No. 9.1e-90;
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Search completed: May 27, 2003, 18:36:27 Job time : 58 secs
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-16
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US-09-904-536-16
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                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09904536 Patent No. US20020111475A1
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT: Graddis, Thomas J.
PPLICANT: McGrew, Jeffrey T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: McGrew, Jeffrey T.
ITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE.
ILE REFERENCE: 03260.0028
                                                           207 WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                     121
                                                                                                                                                  147 RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH 206
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                                                                                                                              RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLPVGLLLLAAAWCLH 180
                                                                                                                                                                                                                                                                  TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 60
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Pred. No. 3.8e-89;
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Pred. No. 1.1e-89;
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US - 08 - 24 - 54.5 - 2
US - 08 - 93 - 66.2 - 2
US - 08 - 20 - 379B - 7
PCT - US94 - 05365 - 17
US - 09 - 109 - 100 - 10
US - 08 - 31 - 522A - 9
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## ALIGNMENTS

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Best Local Similarity 100.0%;
Matches 235; Conservative
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                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/9
FILING DATE: December 18, 1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/08/1
FILING DATE: December 3, 19
                                                                                                                                               APPLICATION NUMBER: 08
FILING DATE: August 12
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: May 24,
CLASSIFICATION: 424
                                                       REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 28:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto:
SOFTWARE: Microsoft Word,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lyman, Stew
APPLICANT: Beckmann, M
TITLE OF INVENTION: L1
NUMBER OF SEQUENCES: 8
                                                                                                              NAME: Malaska, Stephen L
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                   FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 9810
                                     TELEPHONE:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microsoft Word, Version #5:1
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Beckmann, M. Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stephen L. Malaska,
                                       (206)
                                                                                                                                                                                                                                          UMBER: 08/106,463
August 12, 1993
                                                                                                            Stephen
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per 18, 1997
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Patent No.
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Best Local Similarity 100
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
                REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                     FILING DATE: May 24, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                 APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
                                                                                                                                                                                          APPLICATION NUMBER: 08/111,758 FILING DATE: August 25, 1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF
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                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: December
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TELEPHONE:
                                                    REGISTRATION NUMBER:
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                                                                   Malaska, Stephen L.
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beckmann, M. Patricia
VENTION: Ligands for
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-1
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Sequence 6, Application PC/TUS9405365 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Graddis, Thomas J.
APPLICANT: MCGIEW, Jeffrey T.
TITLE OF INVENTION: FLT3-L
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENERAL INFORMATION:
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                                                                                                                            APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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Pred. No. 1.7e-117;
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Best Local (
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                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 756822
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STATE: Washington
               1 MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
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51 University
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                                                            Conservative
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August 12, 1993
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Pred: No. 1
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US-09-109-100-10
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTMARE: PATENTIN VET. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
                                                              Matches
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Best Local
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Best Local Similarity
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 212
                                                                                                                                                                LENGTH: 20
TYPE: PRT
                                                                                                                                            ORGANISM: Homo sapiens
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27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86
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nes 209; Conserv
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APPLICANT: Graddis, Thomas J.

APPLICANT: McGrew, Jeffrey T.

TITLE OF INVENTION: FLI3-L MUTANTS AND METHODS OF USI

FILE REFERENCE: 03260.0028

CURRENT APPLICATION NUMBER: US/09/109,100C

CURRENT FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 9

LENGTH: 209
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                                SEQ ID NO 12
LENGTH: 209
TYPE: PRT
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                                                                                  CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
-09-109-100-12
            ORGANISM: Homo sapiens
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Pred. No. 3e-104;
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US-09-109-100-14
                                                                                                   GENERAL INFORMATION:
                                                                                                                 Sequence 17, Appl. Patent No. 629166
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Best Local Similarity
Matches 208; Conserv
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 209
APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLIT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
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Patent No. 6291661
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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SOFTWARE: PatentIn Ver: 2
SEQ ID NO 11
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LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 17
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUI
FILE REFERENCE: 03260.0028
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                                                   RQNESRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
                                                                    RQNFSRCLELQCQPDSSTLPPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWCLH
                                                                                                                    KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146
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WORTERFIERPGEQVPPVPSPQDLLLVEH
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Pred. No. 4.8e-104;
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Pred. No. 3e-104;
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RESULT 13 US-09-109-100-15 ; Sequence 15, Application US/09109100C ; Patent No. 6291661

181 WQRTRRRTPRPGEQVPPVPSPQDLLLVEH

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; ORGANISM: Homo sapiens
US-09-109-100-15
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Matches
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Applica Patent No. 6291661 GENERAL INFORMATION:
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MU
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                                                                       Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                -09-109-100-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
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EQ ID NO 15
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TYPE: PRT
ORGANISM: Homo sapiens
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207 WORTERFIPERPGEQVPPVPSPQDLLLVEH 235
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                                             RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWC
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Pred. No. 4.8
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 8
LENGTH: 209
TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 208; Conserv
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Patent No. 6291661
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
CURRENT APDITORMON
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APPLICANT: Graddis, Thomas
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 181
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WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                   WORTERFERPGEOVPPVPSPQDLLLVEH 235
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99.5%;
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Pred..No. 7
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